

XX
 XX
 PD 18-APR-1991.
 XX
 PR 25-SEP-1990; 90WO-US05454.
 XX
 PR 26-SEP-1990; 89US-0112745.
 XX
 PA TCELLTM T CELL SCI INC.
 PA KYTO) JOHNS HOPKINS UNIVERSITY.
 PA (BRIG-) BRIGHAM AND WOMEN'S HOSPITAL.
 XX
 PI Fearon DT, Klickstein LB, Wong WW, Carson GR, Hoh M, Concino MF;
 PI Makrides SC, Marsh HC;
 DR WPI; 1991-132854/18.
 DR P-PSDB; AAQ11810.
 XX
 PT Human complement receptor type 1 gene, encoded Proteins and
 PT fragments - for treatment of immune disorders, myocardial infarct,
 PT damage due to inflammation and in treatment of thrombosis
 XX
 PS Claim 1; Fig 1; 23pp; English.
 XX
 This sequence is a composite of sequences isolated as lambda clones
 CC H10.3, T09.1, J3.1 and H7.1. The clones were present in the
 CC specifically primed lambda gt11 cDNA library (Lambda HH) which was
 CC prepared with cDNA synthesised from poly(A)+ RNA from DMSO induced
 CC HL-60 cells. The library was screened using probes CR1-1, CR-2 and
 CC CR1-4 (see Wong WW et al., 1995, Proc. Natl. Acad. Sci. USA, 82:7711)
 CC and probe CR1-18 (corresponding to nucleotides 101-352 of this
 CC sequence). There are four direct, long homologous repeats of 45bp,
 CC each comprising 7 short consensus repeats. Nucleotides 28-1533 are
 CC also claimed separately.
 See also AAQ11813.
 XX
 Sequence 6951 BP; 1802 A; 1681 C; 1659 G; 1809 T; 0 other;
 SQ

alignment_scores:
 Quality: 649.50 Length: 148
 Ratio: 4.883 Gaps: 2
 Percent Similarity: 89.865 Percent Identity: 81.757

alignment_block:
 US-10-031-904-8 x AAQ11642 ..

align seg 1/1 to: AAQ11642 from: 1 to: 6951

10 ProProProSerArgArgPhe....ProLysLeuLeuLeuAlaLalaLe 24
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 70 CCGGCGCCGGTGTCCCTTCGCTCGGAGATCCCTGCAGCGGSGTGT 119

24 uValLeuLeu...LeuSerSerPheSerAspGlnCysAsnValProGlu 40
 ||||| ||||| ||||| ||||| :|||:
 120 GGCGCTGCCTGCCGCTGCCGGTGGCTGGGCAATTGCCCCAGAA 169

40 rProeProPheAlaArgProThrAspLeuThrAspAlaPheGluPhePro 56
 ||||| ||||| ||||| ||||| ||||| :|||:
 170 GGCCTCCCATTTGCCAGGCTTACCACTACTGATGACTTGATTC 219

57 IleGlyThrTyrosAsnTyroGluCysArgProGlyLysArgGlyArgP 73
 ||||| ||||| ||||| ||||| ||||| ||||| :|||:
 220 ATGGGACATATCAGTCAACTGATGAATGCCGCGCCMNGTATTGGAGACC 269

73 OptSerIleLysLeuLysSerValIlePheSerAlaLysAspL 90
 ||||| ||||| ||||| ||||| ||||| :|||:
 270 GTTCTCTTACATCAGCTCAAACATCGCTGAGCTGAGCTGAGCA 319

90 YsCysLysArgLysSerCysArgAsnProProAspProValAsnMet 106
 ||||| :|||:
 320 GGCGAGAGCTAACTACIGCINACCTCCAGATCCAGTGTGATGGATG 369

seq_name: /SIDS1/gcldata/geneseq/geneseqn-emb1/NA1999.DAT:AAZ38150
 seq_documentation_block:
 ID AAZ38150 standard; DNA; 6951 BP.

XX
 AC AAZ38150;
 XX
 DT 22-FEB-2000 (first entry)
 XX
 DE Human C3b/c4b receptor (Crl) protein encoding DNA.
 XX
 KW C3B/C4B receptor; Crl protein; cell-surface protein; erythrocyte; human;
 KW complement regulatory activity; complement pathway enzyme; tissue damage;
 KW reperfusion injury; Arthus reaction; myocardial infarct; inflammation;
 KW heart condition; autoimmune disorder; diagnostic; ss.
 OS Homo sapiens.
 XX
 PN US5981481-A.
 XX
 PD 09-NOV-1999.
 XX
 PR 01-APR-1988; 89US-017552.
 XX
 PF 06-JUN-1995; 95US-0470652.
 XX
 PR 03-APR-1989; 89US-0332865.
 PR 06-DEC-1974; 74US-0350238.
 PR 24-FEB-1993; 93US-0326134.
 PR 09-NOV-1999.
 XX
 PA (NYJO) UNIV JOHNS HOPKINS.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA (AVAN-) AVANT IMMUNOTHERAPEUTICS INC.
 XX
 PI Concino MF, Wong WW, Makrides SC, Klickstein LB, Fearon DT, IP SH;
 PI Marsh HC, Carson GR;
 XX
 DR WPI; 1999-633357/54.
 DR P-PSDB; AAY55751.
 XX
 PT A human C3b/C4b receptor (Crl) protein having antiinflammatory and
 PT cardiant activity -
 XX
 FS Disclosure; fig 1A-P; 87pp; English.
 XX
 The invention relates to a human C3b/C4b receptor (Crl) protein. The Crl
 protein or fragment is expressed as a cell-surface protein on the surface
 of a non-human cell and exhibits a complement regulatory activity of full
 length human Crl as expressed on erythrocytes. The Crl function in vivo
 may be mediated through the inhibition of complement pathway enzymes. The
 soluble Crl protein exhibits a complement regulatory activity, and this
 may be used to prevent reperfusion injury, inhibit Arthus reaction, and
 neutrophil mediated tissue damage, and reduce myocardial infarct size,
 and inflammation. The Crl protein and its fragments can also be used in
 the treatment of conditions which involve unwanted complement activity,
 e.g. shock lung, tissue damage due to burn, or ischemic heart conditions,
 and autoimmune disorders. Crl proteins, analogues, derivatives, and anti-
 Crl antibodies are used in assays, and diagnostics. The present sequence
 represents a DNA encoding the human Crl protein.
 XX
 Sequence 6951 BP; 1802 A; 1680 C; 1661 G; 1808 T; 0 other;

420 TACTAAAGGATACCGACATCATGGTCCCTCGCTGCACATGCATCATCT 469
 140 ergYasnhvalletpaspasnlysthrProvalcSASP 154
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 470 CAGGAGATACTGCTATTGCGATGAAACCATTTGAGAC 513

seq_name: gb_pr:CHPCRIX

seq_documentation_block:

LOCUS CHPCRIX 1985 bp mRNA linear PRI 30-OCT-1994

DEFINITION Pan troglodytes alternatively spliced CRI (CRI) gene, partial cds.

ACCESSION L24921.1 GI:557726

VERSION 1

KEYWORDS alternative splicing product; complement receptor 1.

SOURCE Pan troglodytes

ORGANISM Pan troglodytes

REFERENCE 1 (bases 1 to 1985)
 Birmingham,D.J., Shen,X.P., Hourcade,D., Nickells,M.W. and Atkinson,J.P.

TITLE Primary sequence of an alternatively spliced form of CRI. Candidate for the 75,000 M(r) complement receptor expressed on chimpanzee erythrocytes

JOURNAL J. Immunol. 153 (2), 691-700 (1994)

MEDLINE 94292799

FEATURES source

1. . 1985

/organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /cell_line="EBV transformed"
 /cell_type="B cell"
 /gene="CRI"

sig_peptide

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CDS

<1. . >1985

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 1. . 1985

/gene="CRI"
 51. . 1985

/gene="CRI"
 /product="complement receptor 1"
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mat_peptide

BASE COUNT 521 a 476 c 478 g 510 t

ORIGIN

alignment_scores:

Quality: 645.50 Length: 136 Gaps: 1

Percent Similarity: 50.043 Percent Identity: 86.029

alignment_block: US-10-031-904-8 x CHPCRIX

Align seq 1/1 to: CHPCRIX from: 1 to: 1985

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 |||||:
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6 CTCTGGCGGTGTTGGGCTGCTCTGGCTGCCGCTGGCTGCGCAATG 55
 35 SASVALPROGLUTRPLEAUPOPROHEALARGPROTHRSLNEUTHRSPA 52
 1|||:::|||||:|||||:|||||:|||||:
 56 CAATGCCCGAGATGGCTTCATTGCGCAGGCCAACACCTACTGATG 105
 52 SPHEGLUPHEPROLEGLYTHRTYLeuLeuNTYRGLUCYSATGPROGLY 68
 ::|||||:|||||:|||||:|||||:
 106 AGTTGAGTTCCATGGACATCTGACTATGATGCGGCCGCGT 155
 69 TYSERGLYARPROPHESERIILEIeCysLeuIysAsnSerIamPhe 85
 |||||:|||||:|||||:
 156 TATATGGAGACCGTTCTCATCTGCCTAAAAACTCAGCTGGAC 205
 85 RSERALAYSAPLYSPLYSLYSARVYSSCYSArgAsnProProSP 102
 1:|||||:|||||:
 206 TGTTGCTTGGAGAGGGCAGCAGTATGCGTAACTTCACATC 255
 102 roValAsnGlyMetAlaHisValLeuLysPheIleGlyPheGlySerGln 118
 |||||:|||||:
 256 CTGTTGAATGCGATGCTGTCATGAGCAAGACATCCAACTCGGATCCAA 305
 119 ILeIYStYSeCysProlgyLyrArgLeuIleGlySerSer 135
 |||||:|||||:
 306 ATTAATATCTGTTACTAAAGGATACCGACTCTTGTTCCMGTCTGC 355
 135 ATHCYsIleIleSerGlyAsnHtrValleTPraspNlySthrPro 152
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 356 CACATGCATCATCTGATGACTCTGATGAAACACTA 405
 152 alcYsASP 154
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 406 TTGTGAC 413
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seq_name: gb_pr:CHPCRIWT

seq_documentation_block:

LOCUS CHPCRIWT 6044 bp mRNA linear PRI 30-OCT-1994

DEFINITION Chimpanzee complement receptor type one (CRI) mRNA, partial cds.

ACCESSION L24920.1 GI:551564

KEYWORDS complement receptor 1.

ORGANISM Pan troglodytes

REFERENCE Birmingham,D.J., Shen,X.P., Hourcade,D., Nickells,M.W. and Atkinson,J.P.

TITLE Primary sequence of an alternatively spliced form of CRI. Candidate for the 75,000 M(r) complement receptor expressed on chimpanzee erythrocytes

JOURNAL J. Immunol. 153 (2), 691-700 (1994)

MEDLINE 94292799

FEATURES source

1. . 6044

/organism="Pan troglodytes"
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gene

CDS

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 1. . 1985

/gene="CRI"
 51. . 1985

/gene="CRI"
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mat_peptide

BASE COUNT 521 a 476 c 478 g 510 t

ORIGIN

alignment_scores:

Quality: 645.50 Length: 136 Gaps: 1

Percent Similarity: 50.043 Percent Identity: 86.029

alignment_block: US-10-031-904-8 x CHPCRIWT

Align seq 1/1 to: CHPCRIWT from: 1 to: 1985

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 |||||:
 |||||

QIFCISPPVPIFNGRITKGKLEVPFGKAVNYTDDPHDRGTFDLIGESTRCSDPQ
GNGVWSSPAPRGCGLGHCOAPDRLFLAKTTONASPRCPSTSILKURCRBYGGPS
ITCLONLWSSPKVKCKRSCKPPDPNGMHWIHDIVSRRINVSTCTHRIGHS
SABCILSGNAAHSAKPKCQRCIPLCGLPTIANGDFISTRNRFHGSVWYTCRGPS
RKRYFELVCGERSPCYTSNDQGIVWSPAPOCITPNKCTPENVGLYSDNRFLFS
UNNEVEFRCPGEMAKGPKRVKCALNKWEPPLSCSRVCOPPDYLHARTORKD
NSPOEVFESCPEDLDRGKASLRCTFCODWSAFAPELSCSRVCESCGDMQLAGRYLFP
VNLQGAKVIFVCEGFOKGSSACVLAGMSLWNSSVPCQFCSPVTINGR
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LGACOPRDHLFAKTYNQCPGKAVNYTDDPHDRGTFDLIGESTRCSDPQNGWVWSPAPCGD
VCRKASCKTPDPNGMVWVITDIQVGSIINTSCTGIRLIGHSSCILGSNSHWS
TRPPTCOTRCGGLPANTGDFISTRNRFHGSVWYTCRGPS
VCTSDUDGKTIWSPAPCOTIPNCPTPNVHENGILVSDNLSLFWERFCRQGV
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EGFRUKSSYHCVLGMWSLWNNSVPCQFCOPNPATINGR
ISYTOHPDPRGMENLGESETRCTSDPHNGWVWSPAPCPLYPHAGCKTPQFP
PASPFPDNEFPGVSMCEPGVGMKSISLLENWVSDNLSLFWERFCRQGV
EPPNGAVHNTDGTGTYSCFGRGTSITCLVSGNNVWTMKKAPCICEITSC
RPSPPRCFTTCAKRENAKRGNSFSLTWRFQGWTWASHTQC
NGRMGRKLPICSRVCOPPELHATSHQDSNPSQEVFVSYDQRGAALHC
TPOGWSPEARCVKSCDFLQGPHGRBLTFLNOLQGAKVSKV
HCVTAKMALLANSVWPKCOPDQGKPFVYRFLPGRVYRFLPGRVYRFLP
GWTNIGESSPCTSDPOQNGWVWSPAPCCLSVPACKPHPKIONGDIGHHSLY
LPGMTSYVLCRKGTDYLVGKTFDQGWSQDHYCKEVNSFPFMNGKSLFEMK
KVHYGDYVNLKEDYLVGKTFDQGWSQDHYCKEVNSFPFMNGKSLFEMK
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BASE COUNT 1561 a 1496 c 1162 g 1525 t
ORIGIN

alignment_scores:
 Quality: 645.50 Length: 136
 Ratio: 5.043 Gaps: 1
 Percent Similarity: 94.118 Percent Identity: 86.029

alignment_block:
 US-10-031-904-8 x CHPCR1WT ..

Align seg 1/1 to: CHPCR1WT from: 1 to: 6044

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 6 CTGCTGGCGGTGCGGCGTCGCTGCCCTGGGTCATG 55

35 SASAVLPrglmlPrlgleProPhelaarargProLAsleutamnAspa 52
 ||||:|||||:|||||:|||||:|||||:|||||:|||||:
 56 CAAAGCCAGAGTCGTCATTGCGAGCTACACCTATGAG 105

52 sprngeglueProLgIlyThTyrieAsuAsyTyrglySArgroGly 68
 ||||:|||||:|||||:|||||:|||||:
 106 AGTTTGAGTTCCATGGACATATCATACTATCAGCCCTGGT 155

69 TYSRIGVYLRGProPhSerilelecyseLysAsnSerValTrpTh 85
 |||
 156 TATTTGGAGAACGGTTCTCATCAGTCCTAAACTGCGAC 205

85 rSeRAlaLySAspLySAspLySAspCysAspAsnProProAspP 102
 ||||:|||||:|||||:|||||:|||||:
 206 TGGCTTAAGGAGAGCTGAGCTAACTCTCAAGATC 255

102 rovalasnGlyMetAlaHisValleIysAspIleGlnPheGlySerIin 118
 |||||:|||||:|||||:
 256 CTGCTGGATGCGATGGTCATGTCATCAAAGACATCCAACTGGANCCAA 305

119 IleLysTyrSerCysProLySglYTrgIleLysIleLysSerSerIal 135
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 306 ATTAAATATCTCTGCTTCAAGATTCAGCTTCTGCTGCTG 355

135 atherosystleresergyAsnThrValleIleTrpAspAsnLysIleThrProv 152
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 356 CACAGCATGATCAGGAGTAGCTGATTCAGGATAGCTAACTCTCAAGATC 405

seq_name: gb_pr:hsCR1RS
 seq_documentation_block:
 LOCUS RSCR1RS
 DEFINITION Human mRNA for C3b/C4b receptor secreted form.
 ACCESSION X14362.1
 VERSION X14362.1 GI:30197
 KEYWORDS alternate splicing; C3b/C4b receptor; complement receptor;
 receptor.
 SOURCE human.
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 2376)
 AUTHORS Hourcade,D.
 TITLE Direct Submission
 JOURNAL Submitted (29-NOV-1988) Hourcade D., Howard Hughes Medical Institute, 660 S. Euclid St. Louis Mo, 63110, USA
 REFERENCE 2 (bases 1 to 2376)
 AUTHORS Hourcade,D.R., Atkinson,J.P. and Holes,V.M.
 TITLE Identification of an alternative polyadenylation site in the human C3b/C4b receptor (complement receptor type 1) transcriptional unit and prediction of a secreted form of complement receptor type 1
 J. Exp. Med. 168 (4), 1255-1270 (1988)
 J. Exp. Med. 165:1065-1112(1987) x05309 and in J. Exp. Med. 168:1699-1717(1988)

JOURNAL 89010527
 MEDLINE
 COMMENT The sequence overlaps with that reported by Klickstein et. al. in
 J. Exp. Med. 165:1065-1112(1987) x05309 and in J. Exp. Med. 168:1699-1717(1988)

FEATURES source
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 RGSSVWYTCRGPSGKVKFELVPEPSLCTSNDQGIVWSPAPCOCITENKCTPEN
 ENGLVTSNFSLNEVEFRCPGPMKGRVKQCALNKWEPPLSCSRVCOPP
 DVLAHPTORDKMDNSPGEVFSCPEYDRLRASRHCPTGQDWPAAPCCEVSCE
 DRMGQIQRIFPVLQGAKVDFVCDGFGOKRSSACVLAGMSLWNSSVCE
 QIFCSPSPVTPVINGRKPVEPFKGKAVNYTDDPHDRGTFDLIGESTRCSDPQ
 ICFCISPPVPIFNGRITKGKLEVPFGKAVNYTDDPHDRGTFDLIGESTRCSDPQ
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 406 TTSAGAC 413

alignment_scores:
 Quality: 644.50 Length: 136
 Ratio: 5.035 Gaps: 1
 Percent Similarity: 94.118 Percent Identity: 86.029

alignment_block:
 US-10-031-904-8 x HSCR1RS ..

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7 2002

Align seg i1 to: HSCRIS from: 1 to: 23760

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  55 CAATGCCCGAGATGCTGCCTTCATTTGCCAGGCCTCAACACTACTGATG 105
  52 SPHEGGLUPEHPROLEGLIYTHRYTIEASASYTGGLUCYSASAGPROLY 68
  106 AGTGTGGAGTTCATGAGTGGACATTCGACTCATGATCATGCCGCTGTG 155

```

Protocol:	Template:	25 ng
Primer:	each 1 μ M	
dNTPs:	each 200 μ M	
Taq Polymerase:	0.05 units/ μ l	
Total Vol:	10 μ l	
Buffer:		
MgCl ₂ :	2.5 mM	
KCl:	50 mM	
Tris-HCl:	20 mM	
pH:	8.3	

Prepared with primer pairs provided by Sandoz, derived from x14361
-- Washington University/Merck EST sequence.

FEATURES	SOURCE
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1680 . 1699	
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549 c	568 g
ORIGIN	626 .

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alignment_scores: - Quality: 64.450 Length: 1366
Percent_Similarity: 94.110 Ratio: 5.035 Gaps: 1
alignment_block: -----

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OS-10-031-904-8 x G28591 ..
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 58 sppregIupheeroilegIyThryleasnTgluysargPrGly 68
 59 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 60 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 61 :|||||:|||||:|||||:|||||:|||||:
 62 :|||||:
 63 :
 64 :

JOURNAL COMMENT

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1

Department of Genetics, M-344, Stanford, CA 94305, USA
 Tel: 415/723-9680
 Fax: 415/723-9689
 Email: myersedg@stanford.edu
Primer A: TGAGTGGGAGGACATCTC
Primer B: CATACTCTTATGTCAGTCCTCC
STS size: 216
PCR profile:
 initial incubation: 94 degrees C for 90 second
 Denaturation: 94 degrees C for 15 second
 Annealing: 52 degrees C for 23 second
 Polymerization: 32 degrees C for 30 second
 PCR CYCLES:
 Thermal Cycler:
 Perkin Elmer 9600

102 royalAnGlyMetAlaHisValLeuTyrAspIleuPheGlySerIle 118
 119 HeLsTyR-SerCysProLySProLysGlyLeuIleGlySerSerSerAla 135
 306 ATTAAATATCTGCTGACTAAAGGAAACGACTCATGGTGCTCGTCG 355
 135 aThrCaAIIleIleSerIleAsnTrValIlePheAspAlaLysThrPro 152
 356 CACGACCATCTCAGGTGATACTGGATAATGAAACACCTA 405
 152 aLyGAsP 154
 406 TTTGTCAC 413